

IMMUNEX CORPORATION

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia
- (ii) TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Stephen L. Malaska, Immunex Corporation
 - (B) STREET: 51 University Street
 - (C) CITY: Seattle
 - (D) STATE: Washington
 - (E) COUNTRY: US
 - (F) ZIP: 98101
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: Apple Macintosh
 - (C) OPERATING SYSTEM: Macintosh 7.0.1
 - (D) SOFTWARE: Microsoft Word, Version #5.1
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: -to be assigned-
 - (B) FILING DATE: December 3, 1993
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/111,758
 - (B) FILING DATE: August 25, 1993
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/106,463
 - (B) FILING DATE: August 12, 1993
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/068,394
 - (B) FILING DATE: May 24, 1993
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Malaska, Stephen L.
 - (B) REGISTRATION NUMBER: 32,655
 - (C) REFERENCE/DOCKET NUMBER: 2813-C
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206) 587-0430
 - (B) TELEFAX: (206) 233-0644
 - (C) TELEX: 756822

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 879 base pairs
 - (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..25

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 855..879

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 57..752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | | | | | | |
|---|------------|------------|------------|------------|--------|----|
| GTCGACTGGA | ACGAGACGAC | CTGCTCTGTC | ACAGGCATGA | GGGGTCCCCG | GCAGAG | 56 |
| ATG ACA GTG CTG GCG CCA GCC TGG AGC CCA AAT TCC TCC CTG TTG CTG | 104 | | | | | |
| Met Thr Val Leu Ala Pro Ala Trp Ser Pro Asn Ser Ser Leu Leu Leu | | | | | | |
| 1 5 10 15 | | | | | | |
| CTG TTG CTG CTG CTG AGT CCT TGC CTG CGG GGG ACA CCT GAC TGT TAC | 152 | | | | | |
| Leu Leu Leu Leu Leu Ser Pro Cys Leu Arg Gly Thr Pro Asp Cys Tyr | | | | | | |
| 20 25 30 | | | | | | |
| TTC AGC CAC AGT CCC ATC TCC TCC AAC TTC AAA GTG AAG TTT AGA GAG | 200 | | | | | |
| Phe Ser His Ser Pro Ile Ser Asn Phe Lys Val Lys Phe Arg Glu | | | | | | |
| 35 40 45 | | | | | | |
| TTG ACT GAC CAC CTG CTT AAA GAT TAC CCA GTC ACT GTG GCC GTC AAT | 248 | | | | | |
| Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val Thr Val Ala Val Asn | | | | | | |
| 50 55 60 | | | | | | |
| CTT CAG GAC GAG AAG CAC TGC AAG GCC TTG TGG AGC CTC TTC CTA GCC | 296 | | | | | |
| Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala | | | | | | |
| 65 70 75 80 | | | | | | |
| CAG CGC TGG ATA GAG CAA CTG AAG ACT GTG GCA GGG TCT AAG ATG CAA | 344 | | | | | |
| Gln Arg Trp Ile Glu Gln Leu Lys Thr Val Ala Gly Ser Lys Met Gln | | | | | | |
| 85 90 95 | | | | | | |
| ACG CTT CTG GAG GAC GTC AAC ACC GAG ATA CAT TTT GTC ACC TCA TGT | 392 | | | | | |
| Thr Leu Leu Glu Asp Val Asn Thr Glu Ile His Phe Val Thr Ser Cys | | | | | | |
| 100 105 110 | | | | | | |
| ACC TTC CAG CCC CTA CCA GAA TGT CTG CGA TTC GTC CAG ACC AAC ATC | 440 | | | | | |
| Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile | | | | | | |
| 115 120 125 | | | | | | |

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| | |
|---|-----|
| TCC CAC CTC CTG AAG GAC ACC TGC ACA CAG CTG CTT GCT CTG AAG CCC | 488 |
| Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro | |
| 130 135 140 | |
| TGT ATC GGG AAG GCC TGC CAG AAT TTC TCT CGG TGC CTG GAG GTG CAG | 536 |
| Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln | |
| 145 150 155 160 | |
| TGC CAG CCG GAC TCC TCC ACC CTG CTG CCC CCA AGG AGT CCC ATA GCC | 584 |
| Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala | |
| 165 170 175 | |
| CTA GAA GCC ACG GAG CTC CCA GAG CCT CGG CCC AGG CAG CTG TTG CTC | 632 |
| Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu | |
| 180 185 190 | |
| CTG CTG CTG CTG CTG CCT CTC ACA CTG GTG CTG CTG GCA GCC GCC TGG | 680 |
| Leu Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Ala Trp | |
| 195 200 205 | |
| GGC CTT CGC TGG CAA AGG GCA AGA AGG AGG GGG GAG CTC CAC CCT GGG | 728 |
| Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro Gly | |
| 210 215 220 | |
| GTG CCC CTC CCC TCC CAT CCC TAGGATTCGA GCCTTGTGCA TCGTTGACTC | 779 |
| Val Pro Leu Pro Ser His Pro | |
| 225 230 | |
| AGCCAGGGTC TTATCTCGGT TACACCTGTA ATCTCAGCCC TTGGGAGCCC AGAGCAGGAT | 839 |
| TGCTGAATGG TCTGGAGCAG GTCGTCTCGT TCCAGTCGAC | 879 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | |
|---|--|
| Met Thr Val Leu Ala Pro Ala Trp Ser Pro Asn Ser Ser Leu Leu Leu | |
| 1 5 10 15 | |
| Leu Leu Leu Leu Leu Ser Pro Cys Leu Arg Gly Thr Pro Asp Cys Tyr | |
| 20 25 30 | |
| Phe Ser His Ser Pro Ile Ser Ser Asn Phe Lys Val Lys Phe Arg Glu | |
| 35 40 45 | |
| Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val Thr Val Ala Val Asn | |
| 50 55 60 | |
| Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala | |
| 65 70 75 80 | |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Arg | Trp | Ile | Glu | Gln | Leu | Lys | Thr | Val | Ala | Gly | Ser | Lys | Met | Gln | 85 | 90 | 95 |
| Thr | Leu | Leu | Glu | Asp | Val | Asn | Thr | Glu | Ile | His | Phe | Val | Thr | Ser | Cys | 100 | 105 | 110 |
| Thr | Phe | Gln | Pro | Leu | Pro | Glu | Cys | Leu | Arg | Phe | Val | Gln | Thr | Asn | Ile | 115 | 120 | 125 |
| Ser | His | Leu | Leu | Lys | Asp | Thr | Cys | Thr | Gln | Leu | Leu | Ala | Leu | Lys | Pro | 130 | 135 | 140 |
| Cys | Ile | Gly | Lys | Ala | Cys | Gln | Asn | Phe | Ser | Arg | Cys | Leu | Glu | Val | Gln | 145 | 150 | 155 |
| Cys | Gln | Pro | Asp | Ser | Ser | Thr | Leu | Leu | Pro | Pro | Arg | Ser | Pro | Ile | Ala | 165 | 170 | 175 |
| Leu | Glu | Ala | Thr | Glu | Leu | Pro | Glu | Pro | Arg | Pro | Arg | Gln | Leu | Leu | Leu | 180 | 185 | 190 |
| Leu | Leu | Leu | Leu | Leu | Pro | Leu | Thr | Leu | Val | Leu | Leu | Ala | Ala | Ala | Trp | 195 | 200 | 205 |
| Gly | Leu | Arg | Trp | Gln | Arg | Ala | Arg | Arg | Arg | Gly | Glu | Leu | His | Pro | Gly | 210 | 215 | 220 |
| Val | Pro | Leu | Pro | Ser | His | Pro | | | | | | | | | | 225 | 230 | |

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCGACTGGAA CGAGACGACC TGCT

24

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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| | |
|---|-----|
| CAG CTG GTG GCG CTG AAG CCC TGG ATC ACT CGC CAG AAC TTC TCC CGG | 485 |
| Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg | |
| 140 145 150 | |
| TGC CTG GAG CTG CAG TGT CAG CCC GAC TCC TCA ACC CTG CCA CCC CCA | 533 |
| Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro | |
| 155 160 165 | |
| TGG AGT CCC CGG CCC CTG GAG GCC ACA GCC CCG ACA GCC CCG CAG CCC | 581 |
| Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro | |
| 170 175 180 | |
| CCT CTG CTC CTC CTA CTG CTG CTG CCC GTG GGC CTC CTG CTG CTG GCC | 629 |
| Pro Leu Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala | |
| 185 190 195 200 | |
| GCT GCC TGG TGC CTG CAC TGG CAG AGG ACG CGG CGG AGG ACA CCC CGC | 677 |
| Ala Ala Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg | |
| 205 210 215 | |
| CCT GGG GAG CAG GTG CCC CCC GTC CCC AGT CCC CAG GAC CTG CTG CTT | 725 |
| Pro Gly Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu | |
| 220 225 230 | |
| GTG GAG CAC TGACCTGGCC AAGGCCTCAT CCTGCGGAGC CTTAAACAAC | 774 |
| Val Glu His | |
| 235 | |
| GCAGTGAGAC AGACATCTAT CATCCCATTT TACAGGGGAG GATACTGAGG CACACAGAGG | 834 |
| GGAGTCACCA GCCAGAGGAT GTATAGCCTG GACACAGAGG AAGTTGGCTA GAGGCCGGTC | 894 |
| CCTTCCTTGG GCCCCTCTCA TTCCCTCCCC AGAATGGAGG CAACGCCAGA ATCCAGCACC | 954 |
| GGCCCCATTT ACCCAACTCT GAACAAAGCC CCCG | 988 |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

| | |
|---|--|
| Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu | |
| 1 5 10 15 | |
| Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe | |
| 20 25 30 | |
| Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu | |
| 35 40 45 | |
| Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu | |
| 50 55 60 | |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Asp | Glu | Glu | Leu | Cys | Gly | Gly | Leu | Trp | Arg | Leu | Val | Leu | Ala | Gln | 65 | 70 | 75 | 80 |
| Arg | Trp | Met | Glu | Arg | Leu | Lys | Thr | Val | Ala | Gly | Ser | Lys | Met | Gln | Gly | 85 | 90 | 95 | |
| Leu | Leu | Glu | Arg | Val | Asn | Thr | Glu | Ile | His | Phe | Val | Thr | Lys | Cys | Ala | 100 | 105 | 110 | |
| Phe | Gln | Pro | Pro | Pro | Ser | Cys | Leu | Arg | Phe | Val | Gln | Thr | Asn | Ile | Ser | 115 | 120 | 125 | |
| Arg | Leu | Leu | Gln | Glu | Thr | Ser | Glu | Gln | Leu | Val | Ala | Leu | Lys | Pro | Trp | 130 | 135 | 140 | |
| Ile | Thr | Arg | Gln | Asn | Phe | Ser | Arg | Cys | Leu | Glu | Leu | Gln | Cys | Gln | Pro | 145 | 150 | 155 | 160 |
| Asp | Ser | Ser | Thr | Leu | Pro | Pro | Pro | Trp | Ser | Pro | Arg | Pro | Leu | Glu | Ala | 165 | 170 | 175 | |
| Thr | Ala | Pro | Thr | Ala | Pro | Gln | Pro | Pro | Leu | Leu | Leu | Leu | Leu | Leu | Leu | 180 | 185 | 190 | |
| Pro | Val | Gly | Leu | Leu | Leu | Leu | Ala | Ala | Ala | Trp | Cys | Leu | His | Trp | Gln | 195 | 200 | 205 | |
| Arg | Thr | Arg | Arg | Arg | Thr | Pro | Arg | Pro | Gly | Glu | Gln | Val | Pro | Pro | Val | 210 | 215 | 220 | |
| Pro | Ser | Pro | Gln | Asp | Leu | Leu | Leu | Val | Glu | His | | | | | | 225 | 230 | 235 | |

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|----|
| AATTGGTACC | TTTGGATAAA | AGAGACTACA | AGGACGACGA | TGACAAGACA | CCTGACTGTT | 60 |
| ACTTCAGCCA | C | | | | | 71 |

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(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATATGGATCC CTACTGCCTG GGCCGAGGCT CTGGGAG

37



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia
- (ii) TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Stephen L. Malaska, Immunex Corporation
 - (B) STREET: 51 University Street
 - (C) CITY: Seattle
 - (D) STATE: Washington
 - (E) COUNTRY: US
 - (F) ZIP: 98101
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: Apple Macintosh
 - (C) OPERATING SYSTEM: Macintosh 7.0.1
 - (D) SOFTWARE: Microsoft Word, Version #5.1
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: -to be assigned-
 - (B) FILING DATE: December 3, 1993
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/111,758
 - (B) FILING DATE: August 25, 1993
 - (C) CLASSIFICATION:
- (viii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/106,463
 - (B) FILING DATE: August 12, 1993
 - (C) CLASSIFICATION:
- (ix) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/068,394
 - (B) FILING DATE: May 24, 1993
 - (C) CLASSIFICATION:
- (x) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Malaska, Stephen L.
 - (B) REGISTRATION NUMBER: 32,655
 - (C) REFERENCE/DOCKET NUMBER: 2813-C
- (xi) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206) 587-0430
 - (B) TELEFAX: (206) 233-0644
 - (C) TELEX: 756822

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 879 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..25

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 855..879

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 57..752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|--------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GTCGACTGGA | ACGAGACGAC | CTGCTCTGTC | ACAGGCATGA | GGGGTCCCCG | GCAGAG | 56 | | | | | | | | | | |
| ATG | ACA | GTG | CTG | GCG | CCA | GCC | TGG | AGC | CCA | AAT | TCC | TCC | CTG | TTG | CTG | 104 |
| Met | Thr | Val | Leu | Ala | Pro | Ala | Trp | Ser | Pro | Asn | Ser | Ser | Leu | Leu | Leu | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| CTG | TTG | CTG | CTG | CTG | AGT | CCT | TGC | CTG | CGG | GGG | ACA | CCT | GAC | TGT | TAC | 152 |
| Leu | Leu | Leu | Leu | Leu | Ser | Pro | Cys | Leu | Arg | Gly | Thr | Pro | Asp | Cys | Tyr | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| TTC | AGC | CAC | AGT | CCC | ATC | TCC | TCC | AAC | TTC | AAA | GTG | AAG | TTT | AGA | GAG | 200 |
| Phe | Ser | His | Ser | Pro | Ile | Ser | Ser | Asn | Phe | Lys | Val | Lys | Phe | Arg | Glu | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| TTG | ACT | GAC | CAC | CTG | CTT | AAA | GAT | TAC | CCA | GTC | ACT | GTG | GCC | GTC | AAT | 248 |
| Leu | Thr | Asp | His | Leu | Leu | Lys | Asp | Tyr | Pro | Val | Thr | Val | Ala | Val | Asn | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| CTT | CAG | GAC | GAG | AAG | CAC | TGC | AAG | GCC | TTG | TGG | AGC | CTC | TTC | CTA | GCC | 296 |
| Leu | Gln | Asp | Glu | Lys | His | Cys | Lys | Ala | Leu | Trp | Ser | Leu | Phe | Leu | Ala | |
| 65 | | | | | 70 | | | | 75 | | | | | | 80 | |
| CAG | CGC | TGG | ATA | GAG | CAA | CTG | AAG | ACT | GTG | GCA | GGG | TCT | AAG | ATG | CAA | 344 |
| Gln | Arg | Trp | Ile | Glu | Gln | Leu | Lys | Thr | Val | Ala | Gly | Ser | Lys | Met | Gln | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| ACG | CTT | CTG | GAG | GAC | GTC | AAC | ACC | GAG | ATA | CAT | TTT | GTC | ACC | TCA | TGT | 392 |
| Thr | Leu | Leu | Glu | Asp | Val | Asn | Thr | Glu | Ile | His | Phe | Val | Thr | Ser | Cys | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| ACC | TTC | CAG | CCC | CTA | CCA | GAA | TGT | CTG | CGA | TTC | GTC | CAG | ACC | AAC | ATC | 440 |
| Thr | Phe | Gln | Pro | Leu | Pro | Glu | Cys | Leu | Arg | Phe | Val | Gln | Thr | Asn | Ile | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| TCC | CAC | CTC | CTG | AAG | GAC | ACC | TGC | ACA | CAG | CTG | CTT | GCT | CTG | AAG | CCC | 488 |
| Ser | His | Leu | Leu | Lys | Asp | Thr | Cys | Thr | Gln | Leu | Leu | Ala | Leu | Lys | Pro | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |

| | | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|---------|------|------------|------------|-----|-----|-----|-----|-----|-----|
| TGT | ATC | GGG | AAG | GCC | TGC | CAG | AAT | TTC | TCT | CGG | TGC | CTG | GAG | GTG | CAG | 536 |
| Cys | Ile | Gly | Lys | Ala | Cys | Gln | Asn | Phe | Ser | Arg | Cys | Leu | Glu | Val | Gln | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| TGC | CAG | CCG | GAC | TCC | TCC | ACC | CTG | CTG | CCC | CCA | AGG | AGT | CCC | ATA | GCC | 584 |
| Cys | Gln | Pro | Asp | Ser | Ser | Thr | Leu | Leu | Pro | Pro | Arg | Ser | Pro | Ile | Ala | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| CTA | GAA | GCC | ACG | GAG | CTC | CCA | GAG | CCT | CGG | CCC | AGG | CAG | CTG | TTG | CTC | 632 |
| Leu | Glu | Ala | Thr | Glu | Leu | Pro | Glu | Pro | Arg | Pro | Arg | Gln | Leu | Leu | Leu | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| CTG | CTG | CTG | CTG | CTG | CCT | CTC | ACA | CTG | GTG | CTG | CTG | GCA | GCC | GCC | TGG | 680 |
| Leu | Leu | Leu | Leu | Leu | Pro | Leu | Thr | Leu | Val | Leu | Leu | Ala | Ala | Ala | Trp | |
| | | | 195 | | | | 200 | | | | | 205 | | | | |
| GGC | CTT | CGC | TGG | CAA | AGG | GCA | AGA | AGG | AGG | GGG | GAG | CTC | CAC | CCT | GGG | 728 |
| Gly | Leu | Arg | Trp | Gln | Arg | Ala | Arg | Arg | Arg | Gly | Glu | Leu | His | Pro | Gly | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| GTG | CCC | CTC | CCC | TCC | CAT | CCC | TAGGATT | TCGA | GCCTTGTGCA | TCGTTGACTC | | | | | | 779 |
| Val | Pro | Leu | Pro | Ser | His | Pro | | | | | | | | | | |
| 225 | | | | | 230 | | | | | | | | | | | |
| AGCCAGGGTC | TTATCTCGGT | TACACCTGTA | ATCTCAGCCC | TTGGGAGCCC | AGAGCAGGAT | | | | | | | | | | | 839 |
| TGCTGAATGG | TCTGGAGCAG | GTCGTCTCGT | TCCAGTCGAC | | | | | | | | | | | | | 879 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Thr | Val | Leu | Ala | Pro | Ala | Trp | Ser | Pro | Asn | Ser | Ser | Leu | Leu | Leu | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Leu | Leu | Leu | Leu | Leu | Ser | Pro | Cys | Leu | Arg | Gly | Thr | Pro | Asp | Cys | Tyr | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Phe | Ser | His | Ser | Pro | Ile | Ser | Ser | Asn | Phe | Lys | Val | Lys | Phe | Arg | Glu | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Leu | Thr | Asp | His | Leu | Leu | Lys | Asp | Tyr | Pro | Val | Thr | Val | Ala | Val | Asn | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Leu | Gln | Asp | Glu | Lys | His | Cys | Lys | Ala | Leu | Trp | Ser | Leu | Phe | Leu | Ala | |
| 65 | | | | 70 | | | | | 75 | | | | | | 80 | |
| Gln | Arg | Trp | Ile | Glu | Gln | Leu | Lys | Thr | Val | Ala | Gly | Ser | Lys | Met | Gln | |
| | | | 85 | | | | | 90 | | | | | | 95 | | |
| Thr | Leu | Leu | Glu | Asp | Val | Asn | Thr | Glu | Ile | His | Phe | Val | Thr | Ser | Cys | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |

Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile
 115 120 125
 Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro
 130 135 140
 Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln
 145 150 155 160
 Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala
 165 170 175
 Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu
 180 185 190
 Leu Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Ala Trp
 195 200 205
 Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro Gly
 210 215 220
 Val Pro Leu Pro Ser His Pro
 225 230

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCGACTGGAA CGAGACGACC TGCT

24

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGCAGGTCGT CTCGTTCCAG

20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 988 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 30..734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | | | | | | | | | | | | | | | | |
|------------|------------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CGGCCGGAAT | TCCGGGGCCC | CCGGCCGAA | ATG | ACA | GTG | CTG | GCG | CCA | GCC | TGG | | 53 | | | | |
| | | | Met | Thr | Val | Leu | Ala | Pro | Ala | Trp | | | | | | |
| | | | 1 | | | | 5 | | | | | | | | | |
| AGC | CCA | ACA | ACC | TAT | CTC | CTC | CTG | CTG | CTG | CTG | AGC | TCG | GGA | CTC | 101 | |
| Ser | Pro | Thr | Thr | Tyr | Leu | Leu | Leu | Leu | Leu | Leu | Ser | Ser | Gly | Leu | | |
| | 10 | | | | | 15 | | | | 20 | | | | | | |
| AGT | GGG | ACC | CAG | GAC | TGC | TCC | TTC | CAA | CAC | AGC | CCC | ATC | TCC | TCC | GAC | 149 |
| Ser | Gly | Thr | Gln | Asp | Cys | Ser | Phe | Gln | His | Ser | Pro | Ile | Ser | Ser | Asp | |
| | 25 | | | | 30 | | | | | 35 | | | | | 40 | |
| TTC | GCT | GTC | AAA | ATC | CGT | GAG | CTG | TCT | GAC | TAC | CTG | CTT | CAA | GAT | TAC | 197 |
| Phe | Ala | Val | Lys | Ile | Arg | Glu | Leu | Ser | Asp | Tyr | Leu | Leu | Gln | Asp | Tyr | |
| | | | | 45 | | | | | 50 | | | | | 55 | | |
| CCA | GTC | ACC | GTG | GCC | TCC | AAC | CTG | CAG | GAC | GAG | GAG | CTC | TGC | GGG | GGC | 245 |
| Pro | Val | Thr | Val | Ala | Ser | Asn | Leu | Gln | Asp | Glu | Glu | Leu | Cys | Gly | Gly | |
| | | | 60 | | | | | 65 | | | | | 70 | | | |
| CTC | TGG | CGG | CTG | GTC | CTG | GCA | CAG | CGC | TGG | ATG | GAG | CGG | CTC | AAG | ACT | 293 |
| Leu | Trp | Arg | Leu | Val | Leu | Ala | Gln | Arg | Trp | Met | Glu | Arg | Leu | Lys | Thr | |
| | | 75 | | | | | 80 | | | | | 85 | | | | |
| GTC | GCT | GGG | TCC | AAG | ATG | CAA | GGC | TTG | CTG | GAG | CGC | GTG | AAC | ACG | GAG | 341 |
| Val | Ala | Gly | Ser | Lys | Met | Gln | Gly | Leu | Leu | Glu | Arg | Val | Asn | Thr | Glu | |
| | 90 | | | | | 95 | | | | | 100 | | | | | |
| ATA | CAC | TTT | GTC | ACC | AAA | TGT | GCC | TTT | CAG | CCC | CCC | CCC | AGC | TGT | CTT | 389 |
| Ile | His | Phe | Val | Thr | Lys | Cys | Ala | Phe | Gln | Pro | Pro | Pro | Ser | Cys | Leu | |
| 105 | | | | | 110 | | | | | 115 | | | | | 120 | |
| CGC | TTC | GTC | CAG | ACC | AAC | ATC | TCC | CGC | CTC | CTG | CAG | GAG | ACC | TCC | GAG | 437 |
| Arg | Phe | Val | Gln | Thr | Asn | Ile | Ser | Arg | Leu | Leu | Gln | Glu | Thr | Ser | Glu | |
| | | | | 125 | | | | | 130 | | | | | 135 | | |
| CAG | CTG | GTG | GCG | CTG | AAG | CCC | TGG | ATC | ACT | CGC | CAG | AAC | TTC | TCC | CGG | 485 |
| Gln | Leu | Val | Ala | Leu | Lys | Pro | Trp | Ile | Thr | Arg | Gln | Asn | Phe | Ser | Arg | |
| | | | 140 | | | | | 145 | | | | | 150 | | | |
| TGC | CTG | GAG | CTG | CAG | TGT | CAG | CCC | GAC | TCC | TCA | ACC | CTG | CCA | CCC | CCA | 533 |
| Cys | Leu | Glu | Leu | Gln | Cys | Gln | Pro | Asp | Ser | Ser | Thr | Leu | Pro | Pro | Pro | |
| | | 155 | | | | | 160 | | | | | | 165 | | | |

TGG AGT CCC CGG CCC CTG GAG GCC ACA GCC CCG ACA GCC CCG CAG CCC 581
 Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro
 170 175 180

CCT CTG CTC CTC CTA CTG CTG CTG CCC GTG GGC CTC CTG CTG CTG GCC 629
 Pro Leu Leu Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala
 185 190 195 200

GCT GCC TGG TGC CTG CAC TGG CAG AGG ACG CGG CGG AGG ACA CCC CGC 677
 Ala Ala Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg
 205 210 215

CCT GGG GAG CAG GTG CCC CCC GTC CCC AGT CCC CAG GAC CTG CTG CTT 725
 Pro Gly Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu
 220 225 230

GTG GAG CAC TGACCTGGCC AAGGCCTCAT CCTGCGGAGC CTTAAACAAC 774
 Val Glu His
 235

GCAGTGAGAC AGACATCTAT CATCCCATTT TACAGGGGAG GATACTGAGG CACACAGAGG 834

GGAGTCACCA GCCAGAGGAT GTATAGCCTG GACACAGAGG AAGTTGGCTA GAGGCCGGTC 894

CCTTCCTTGG GCCCCTCTCA TTCCCTCCCC AGAATGGAGG CAACGCCAGA ATCCAGCACC 954

GGCCCCATTT ACCCAACTCT GAACAAAGCC CCCG 988

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
 1 5 10 15

Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
 20 25 30

Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
 35 40 45

Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
 50 55 60

Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
 65 70 75 80

Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
 85 90 95

Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
 100 105 110

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Phe | Gln | Pro | Pro | Pro | Ser | Cys | Leu | Arg | Phe | Val | Gln | Thr | Asn | Ile | Ser | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Arg | Leu | Leu | Gln | Glu | Thr | Ser | Glu | Gln | Leu | Val | Ala | Leu | Lys | Pro | Trp | |
| | | 130 | | | | 135 | | | | | 140 | | | | | |
| Ile | Thr | Arg | Gln | Asn | Phe | Ser | Arg | Cys | Leu | Glu | Leu | Gln | Cys | Gln | Pro | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Asp | Ser | Ser | Thr | Leu | Pro | Pro | Pro | Trp | Ser | Pro | Arg | Pro | Leu | Glu | Ala | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Thr | Ala | Pro | Thr | Ala | Pro | Gln | Pro | Pro | Leu | Leu | Leu | Leu | Leu | Leu | Leu | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Pro | Val | Gly | Leu | Leu | Leu | Leu | Ala | Ala | Ala | Trp | Cys | Leu | His | Trp | Gln | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Arg | Thr | Arg | Arg | Arg | Thr | Pro | Arg | Pro | Gly | Glu | Gln | Val | Pro | Pro | Val | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Pro | Ser | Pro | Gln | Asp | Leu | Leu | Leu | Val | Glu | His | | | | | | |
| 225 | | | | | 230 | | | | | 235 | | | | | | |

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | |
|---|----|
| AATTGGTACC TTTGGATAAA AGAGACTACA AGGACGACGA TGACAAGACA CCTGACTGTT | 60 |
| ACTTCAGCCA C | 71 |

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATATGGATCC CTACTGCCTG GGCCGAGGCT CTGGGAG

37